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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/076,421

DATE: 05/30/2002
TIME: 10:06:16

Input Set : A:\Hayak-9.app
Output Set: N:\CRF3\05302002\J076421.raw

3 <110> APPLICANT: WADA, MANABU
4 WADA, NAOKO
6 <120> TITLE OF INVENTION: ANTI-HIV AGENTS
8 <130> FILE REFERENCE: HAYAK-9
10 <140> CURRENT APPLICATION NUMBER: 10/076,421
C--> 11 <141> CURRENT FILING DATE: 2002-05-17
13 <150> PRIOR APPLICATION NUMBER: JP 2001-42655
14 <151> PRIOR FILING DATE: 2001-02-20
16 <150> PRIOR APPLICATION NUMBER: JP 2001-184284
17 <151> PRIOR FILING DATE: 2001-06-19
19 <160> NUMBER OF SEQ ID NOS: 5
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1296
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
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29 <221> NAME/KEY: CDS
30 <222> LOCATION: (1)..(1293)
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35 1 5 10 15
37 gac tcc aaa ggc agc aat gaa ctt cat caa gtt cca tcg aac tgt gac 96
38 Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp
39 20 25 30
41 tgt cta aat gga gga aca tgt gtg tcc aac aag tac ttc tcc aac att 144
42 Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile
43 35 40 45
45 cac tgg tgc aac tgc cca aag aaa ttc gga ggg cag cac tgt gaa ata 192
46 His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile
47 50 55 60
49 gat aag tca aaa acc tgc tat gag ggg aat ggt cac ttt tac cga gga 240
50 Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly
51 65 70 75 80
53 aag gcc agc act gac acc atg ggc cgg ccc tgc ctg ccc tgg aac tct 288
54 Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser
55 85 90 95
57 gcc act gtc ctt cag caa acg tac cat gcc cac aga tct gat gct ctt 336
58 Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu
59 100 105 110
61 cag ctg ggc ctg ggg aaa cat aat tac tgc agg aac cca gac aac cgg 384
62 Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg

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63	115	120	125	
65	agg cga ccc tgg tgc tat gtg cag gtg ggc cta aag ccg ctt gtc caa			432
66	Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln			
67	130	135	140	
69	gag tgc atg gtg cat gac tgc gca gat gga aaa aag ccc tcc tct cct			480
70	Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro			
71	145	150	155	160
73	cca gaa gaa tta aaa ttt cag tgt ggc caa aag act ctg agg ccc cgc			528
74	Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg			
75	165	170	175	
77	ttt aag att att ggg gga gaa ttc acc acc atc gag aac cac ccc tgg			576
78	Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp			
79	180	185	190	
81	ttt gcg gcc atc tac agg agg cac cggt ggg ggc tct gtc acc tac gtg			624
82	Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val			
83	195	200	205	
85	tgt gga ggc agc ctc atc agc cct tgc tgg gtg atc agc gcc aca cac			672
86	Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His			
87	210	215	220	
89	tgc ttc att gat tac cca aag aag gag gac tac atc gtc tac ctg ggt			720
90	Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly			
91	225	230	235	240
93	cgc tca agg ctt aac tcc aac acg caa ggg gag atg aag ttt gag gtg			768
94	Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val			
95	245	250	255	
97	gaa aac cta atc cta cac aag gac tac agc gct gac acg ctt gct cac			816
98	Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His			
99	260	265	270	
101	cac aac gac att gcc ttg ctg aag atc cgt tcc aag gag ggc agg tgt			864
102	His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys			
103	275	280	285	
105	gcg cag cca tcc cgg act ata cag acc atc tgc ctg ccc tcg atg tat			912
106	Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr			
107	290	295	300	
109	aac gat ccc cag ttt ggc aca agc tgt gag atc act ggc ttt gga aaa			960
110	Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys			
111	305	310	315	320
113	gag aat tct acc gac tat ctc tat ccg gag cag ctg aaa atg act gtt			1008
114	Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val			
115	325	330	335	
117	gtg aag ctg att tcc cac cgg gag tgt cag cag ccc cac tac tac ggc			1056
118	Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly			
119	340	345	350	
121	tct gaa gtc acc acc aaa atg ctg tgt gct gac cca cag tgg aaa			1104
122	Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys			
123	355	360	365	
125	aca gat tcc tgc cag gga gac tca ggg gga ccc ctc gtc tgt tcc ctc			1152
126	Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu			
127	370	375	380	

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129 caa ggc cgc atg act ttg act gga att gtg agc tgg ggc cgt gga tgt 1200
130 Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys
131 385 390 395 400
133 gcc ctg aag gac aag cca ggc gtc tac acg aga gtc tca cac ttc tta 1248
134 Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu
135 405 410 415
137 ccc tgg atc cgc agt cac acc aag gaa gag aat ggc ctg gcc ctc tga 1296
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151 Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp
152 20 25 30
154 Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile
155 35 40 45
157 His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile
158 50 55 60
160 Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly
161 65 70 75 80
163 Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser
164 85 90 95
166 Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu
167 100 105 110
169 Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg
170 115 120 125
172 Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln
173 130 135 140
175 Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro
176 145 150 155 160
178 Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg
179 165 170 175
181 Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp
182 180 185 190
184 Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val
185 195 200 205
187 Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His
188 210 215 220
190 Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly
191 225 230 235 240
193 Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val
194 245 250 255
196 Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His
197 260 265 270
199 His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys

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200 275 280 285
202 Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr
203 290 295 300
205 Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys
206 305 310 315 320
208 Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val
209 325 330 335
211 Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly
212 340 345 350
214 Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys
215 355 360 365
217 Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu
218 370 375 380
220 Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly..Cys
221 385 390 395 400
223 Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu
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226 Pro Trp Ile Arg Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
227 420 425 430
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232 <211> LENGTH: 4
233 <212> TYPE: PRT
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252 <211> LENGTH: 10
253 <212> TYPE: PRT
254 <213> ORGANISM: Homo sapiens
256 <400> SEQUENCE: 5
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VERIFICATION SUMMARY

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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date